STIC-Biotech/ChemLib

74282

From:

Sent:

Seharaseyon, Jegatheesan Wednesday, December 14, 2005 5:15 PM STIC-Biotech/ChemLib

To:

Subject:

Re: 10/084706

Hi,

Please search SEQ ID NO: 2 of 10/084706.

Thanks.

J.Seharaseyon Art Unit 1647 Remsen 4C61 Mailbox 4C70

Phone: (571)-272-0892 Fax: (571)-273-0892

Searcher:	
Searcher Phone:	
Date Searcher Picked up:	
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NA#	AA#:
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endors and cost where applicable
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WWW/Internet:
Other (Specify):

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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felis silve
bos taurus
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ALIGNMENTS

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NUCLEOTIDE SEQUENCE.
MEDLINE=81053722; PubMed=6159584;
Goeddel D.V., Shepard H.M., Yelverton E., Leung D., Crea R., Sloma A.,
Pestka S.;
                                                                                                                                       Name=IFNB1; Synonyms=IFB, IFNB;
Homo sapiens (Human)
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Ammmalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
MEDLINE=81198952; PubMed=6164984;
Lawn R.M., Adelman J., Franke A.E., Houck C.M., Gross M., Najarian R.,
Goeddel D.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
MEDLINE-81.005095; PubMed=6157601; DOI=10.1016/0378-1119(80)90138-9;
Taniguchi T., Ohno S., Fujii-Kuriyama Y., Muramatsu M.;
"The nucleotide sequence of human fibroblast interferon cDNA.";
Gene 10:11-15(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete amino acid sequence of human fibroblast interferon as deduced using synthetic oligodeoxyribonucleotide primers of reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Isolation and structure of a human fibroblast interferon gene."; Nature 285:542-547(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
MEDLINE-80254545; PubMed-6157094;
Derynck R., Content J., Declercq E., Volckaert G., Tavernier J.,
Devos R., Fiers W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
MRDILIBE-81063-770; PubMed=6159580;
MRDILIBE-81063-770; PubMed=6159580;
MNA.W., Stewart A.G., Smith J.C., Doel S.M.,
Houghton M., Eaton M.A.W., Patel T.P., Emtage J.S., Carey N.H.,
Cartlin G.H., Lewis H.M., Patel T.P., Emtage J.S., Carey N.H.,
                                                                                                                                                                                                                                                                                                                                                                                               NUCLECTIDE SEQUENCE.
Ohno S., Taniguchi T.,
"Structure of a chromosomal gene for human interferon beta.";
Proc. Natl. Acad. Sci. U.S.A. 78:5305-5309(1981).
                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Interferon beta precursor (IFN-beta) (Fibroblast interferon)
                                                                                                                                                                                                                                                                                                                                   "Human fibroblast interferon gene lacks introns.";
Nucleic Acids Res. 9:1045-1052(1981).
                              187 AA
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                               PRT;
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                            IFNB HUMAN
P01574;
             I FNB HUMAN
RESULT 1
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NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

NA Straubberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,

Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,

And Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Aspleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toobhiyuti S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Toobhiyuti S., Carninci P., Prange C.,

Raba S.S., McChan P.J., McKernan R.J., Malek J.A., Gunaarane P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

And Halton D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia B.J., Lu X., Gibbs R.A.,

Richards S., Worley W., Sodergren B.J., Lu X., Gibbs R.A.,

Rahting M., Madan A., Young A.C., Shevychenko Y., Bouffard G.G.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S. M., Krzywinski M.I., Skalska U., Smailus D.E.,

Radriguez A.D., Schein J.E., Jones S.J.M., Marra M.A.;

"And mouse Chna Accident Relation on the Initial analysis of more than 15,000 full-length human
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MEDLINE=98004481; PUBMG=934232) DOI=10.1073/pnas.94.22.11813;
Karpusas M., Nolte M., Benton C.B., Maier W., Lipscomb W.N., Goelz S.;
"The crystal structure of human interferon beta at 2.2-A resolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 94:11813-11818 (1997).
-!- FUNCTION: Has antiviral, antibacterial and anticancer activities.
-!- SUBUNIT: Monomer.
-!- SUBCELLULAR LOCATION: Secreted.
-!- PHARMACEUTICAL: Available under the names Avonex (Biogen),
Betaseron (Berlex) and Rebif (Serono). Used in the treatment of
multiple sclerosis (MS). Betaseron is a slightly modified form of
                                                               NUCLEOTIDE SEQUENCE.
MEDLINE=86035565; PubMed=2414376;
May L.T., Sehgal P.B.;
"On the relationship between human interferon alpha 1 and beta 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Houghton M., Stewart A.G., Doel S.M., Emtage J.S., Eaton M.A.W., Smith J.C., Patel T.P., Lewis H.M., Porter A.G., Birch J.R., Cartwright T., Carey N.H.;
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Shepard H.M., Leung D., Stebbing N., Goeddel D.V.;
"A single amino acid change in IFN-betal abolishes its antiviral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Assignment of the disulphide bonds of leukocyte interferon."; Nature 289:606-607(1981).
"Synthesis of human fibroblast interferon by E. coli."; Nucleic Acids Res. 8:4057-4074(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE OF 71-187 (VARIANT CLONE PF526).
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                                                                                                                                                                                     Interferon Res. 5:521-526(1985).
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IFNB1 with two residue substitutions.

SIMILARITY: Belongs to the alpha/beta interferon family.

DATABASE: NAME=Avonex; NOTE=Clinical information on Avonex;

WWW="http://www.avonex.com/msavProject/avonex.portal".

DATABASE: NAME=Betaseron; NOTE=Clinical information on Betaseron;

WWW="http://www.betaseron.com/betas/index.jsp".

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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GO:0005132; F:interferon-alpha/beta receptor binding; NAS.
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ProDom; PD000550; Interferon abd; 1.
PROSITE; PS00252; INTERFERON_A_B_D; 1.
3D-structure; Antivitral defense; Cytokine; Glycoprotein; Pharmaceutical; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-linked (GlcNAc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interferon beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                              EMBL; V00534; CAA23795.1; -; Genomic_DNA.
EMBL; V00535; CAA23796.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                   PDB; 1AU1; X-ray; A/B=22-187.
Ensembl; ENSG0000171855; Homo sapiens.
                                                                                                                                                                                                                             EMBL, BC069314; AAH69314'1; -; MENA.
EMBL, M28622; AAA36040.1; -; MENA.
PIR; A93721; IVHUB1
                                                                                                                                                                                         CAA23807.1; -; mRNA.
                                                                                                                                                                                                                CAA23808.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00143; Interferon; 1
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                                                                                                                                                                                                                                                                                                                                            HGNC; HGNC:5434; IFNB1.
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101
162
162
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187 AA;
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101
52
162
                                                                                                                                                                                         EMBL; V00546;
EMBL; V00547;
                                                                                                                                                                                                                                                                                                                                                                     MIM; 147640;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
DISULFID
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                                                                                                        removed.
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81

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TRUSUBE-PCK rescued clones.

TRUSINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Rausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,

Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., McWam P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Makealey R.W., Touchman J.W., Green E.D., Dickson M.C.,

Radriquez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; BC096151; AAH96152.1; -; mRNA.
EMBL; BC096152; AAH96152.1; -; mRNA.
EMBL; BC096150; AAH96153.1; -; mRNA.
EMBL; BC096150; AAH96150.1; -; mRNA.
Ensembl; RNGG00000171855; Homo sapiens.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005126; F:hemacopoiein/interferon-class (D200-domain. ..; IEA.
GO; GO:0006952; P:defense response; IEA.
                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLUIAR LOCATION: Secreted (By similarity).
EMBL; AL390882; CAH70160.1; -; Genomic_DNA.
EMBL; BC096151; AAH96151.1; -; MRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Martin S.;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22294 MW; 0B013D4087723CEC CRC64;
                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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100.0%; Pred. No. 1.7e-63;
ive 0; Mismatches 0;
                            187 AA
                                                                                                                                                                                           Interferon, beta 1, fibroblast.
Name=IFNB1; ORFNames=RP11-113D19.1-002;
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                                                                                               Created)
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SMART; SM00076; IFabd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       defense; Cytokine
                                                                                                                            (TrEMBLrel. 29, (TrEMBLrel. 31,
                                                                                        01-FEB-2005 (TrEMBLrel. 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00143; Interferon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=PCR rescued clones;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=PCR rescued clones;
                     QSVWC9, HUMAN PRELIMINARY;
QSVWC9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.
                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                            01-FEB-2005
13-SEP-2005
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HUMAN
                               SOW BRANCH BRANC
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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22 MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSYNLLGFLQRSSNFQCQXLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
                                  61 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLBEKLBKEDFTRGKLMSSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hum. Gene Ther. 10:429-440(1999).
-!- FUNCTION: Has antiviral, antibacterial and anticancer activities.
-!- SUBUNIT: Monomer (By similarity).
-!- SUBCILITAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the alpha/beta interferon family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                              Name=IFNB1; Synonyms=IFNB;
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLECTIDE SEQUENCE.
MEDLINE=99156140; PubMed=10048395; DOI=10.1089/10430349950018878;
Matheux F., Le Grand R., Rousseau V., De Maeyer E., Dormont D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . .) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expressed
to SIVmac251
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                                                                                                                       142 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLIGYLRN 187
                                                                                                     121 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.2%; Score 832; DB 1; Length 18° 94.0%; Pred. No. 4.6e-60; Live 7; Mismatches 3; Indels
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N-linked (GlCNAc. . .) (Pc
By similarity.
; 376AEF73332B7807 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Macaque lymphocytes transduced by a constitutively interferon beta gene display an enhanced resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; Fuluescott, 1.

PRART; SMO0176; IFabd; 1.

PROSITE; PS00125; INTERPERON A B D; 1.

Antiviral defense; Cytokine; Glycoprotein; Signal.

Antiviral defense; Cytokine; By Similarity.

21 By Similarity.
                                                                                                                                                                                                                                                              10-MAY-2005 (Rel. 47, Created)
10-MAY-2005 (Rel. 47, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ011909; CAA09862.1; -; Genomic_DNA.
HSSP; P01574; IAU1.
InterPro; IPR000471; Interferon_abd.
PANTHER; PTHR11691; Interferon_abd; 1.
Pfam; PF00143; Interferon; 1.
                                                                                                                                                                                                                                                                                                                                                                                                      Cercopithecidae; Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                 Interferon beta precursor (IFN-beta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PD000550; Interferon_abd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22266 MW;
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                                                                                                                                                                                                                                STANDARD;
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162
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101
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Matches 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infection."
                                                                                                                                                                                                                              IFNB MACFA
077812;
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1 MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRWNFDIPEEIKQLQQFQKEDAALTIY

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· And A. A. A. A. A.

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Indels

Matches 166; Conservative

Local Similarity

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TISSUE=Blood;
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                                                                                                                                                                                                                                                                                                                                                                                           .; IEA.
                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 MSYNLLGFLQRSSNCQCQKLLMQLNGRLEYCLKDRRNFDIPEEIKQLQQFQKEDAAVTIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQXEDAALTIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Interferon-beta-1 precursor (Interferon-beta).
Name=interferon-beta-1; Synonyms=interferon-beta/ polFN-beta;
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                       "The human fibroblast and human immune interferon genes and their
                                                                                                                                                                                                                                                                                                                                                                           GOS (0005576; C:extracellular region; IEA.
GO) GO:0005126; F:hematopoietin/interferon-class (D200-domain. GO) GO:0005126; F:hematopoietin/interferon-class (D200-domain. GO) GO:0006952; F:defense response; IEA.
InterPro; IPR000471; Interferon_abd.
Pfam; PF00143; Interferon; 1.
PRINTS; PR00266; INTERFERONAB.
Probom; PD000550; Interferon_abd; 1.
PROSITE; PS000252; INTERPERON A B D; UNKNOWN 1.
Antiviral defense; Cytokine; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
MEDLINE=83065590; PubMed=6183692;
Fiers W., Remaut E., Devos R., Cheroutre H., Contreras R.R.,
Gheysen D., Degrave W.M., Stanssens P., Tavernier J., Taya Y.,
Content J.;
                                                                                                                                                                                                                                                                                                                   expression in homologous and heterologous cells.";
Philos. Trans. R. Soc. Lond., B, Biol. Sci. 299:29-38(1982).
-!- SUBCELLULAR LOCATION: Secreted (By similarity).
              142 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILENPFFINKLTGYLRN 187
 121 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 827; DB 2; Length 187;
Pred. No. 1.2e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 HLKRYYGRILHYYLKAKEDSHCAWTIVRVEILRNFYVINRLTGYLRN 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 Potential.
187 interferon-beta.
22251 MW; D8EE65B694862061 CRC64;
                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                        187
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                                                                                                              Created)
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                                                                                                                                                                                                                                                                                                                                                       EMBL; M25460; AAC41702.1; -; mRNA.
HSSP; P01574; 1AU1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94.6%;
95.8%;
                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                            01-NOV-1996 (TrEMBLrel. 01,
                                                                                                                                                  Interferon-beta precursor.
                                                                                      Q15943 HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 95.8
Matches 159; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q29412_PIG PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q29412;
01-NOV-1996 (TrEMBLrel.
                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187 AA;
                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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Best Local S
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PIG
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EMLONIFAIFRODSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120
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"Clone and analysis of meishan porcine interferon beta gene.";
"Clone and analysis of meishan porcine interferon beta gene.";
Submitted (UUL-2004) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Secreted (By similarity).
EMBL; AY6872B1, AAT98375.1; -; mRNA.
GO; GO:000576; C:extracellular region; IEA.
GO; GO:0005126; F:hematopoietin/interferon-class (D200-domain. .; IEA.
GO; GO:0006952; P:defense response; IEA.
InterPro; IPR000471; Interferon_abd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .; IEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae;
                                                                                                                                                                                                                                                                  MEDLINE=92348930; Pubmed=1640116; MEDLINE=92348930; Pubmed=1640116; Metureson K., Gobl A., Linderson M., Johansson M., Alm G.; Artureson K., Gobl A., Linderson M., Johansson M., Alm G.; Molecular cloning of a gene encoding porcine interferon-beta."; J. Interferon Res. 12:153-160(1992).

J. Interferon Res. 12:153-160(1992).

- SUBCELLULAR LOCATION: Secreted (By similarity).

EMBL; MG5762; AAA31056.1; -; Genomic_DNA.

HSSP; P01574; AAB22723.1; -; Genomic_DNA.

HSSP; P01574; AAU.

GO; GO:0005575; C:extracellular region; IEA.

GO; GO:0005525; P:defense response; IEA.
                                                                                                                    Johansson M., Alm G.;
porcine interferon-beta.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ۲;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.3%; Score 535.5; DB 2; Length 62.0%; Pred. No. 7.4e-36; rive 28; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probom; PD000550; Interferon abd; 1.
SWART; SM00076; IFabd; 1.
Antiviral defense; Cytokine; Signal.
SIGNAL 1 21 Potential.
22 B0 Potential.
SEQUENCE 186 AA; 21878 MW; 5F16B8B3C3AE603D CRC64;
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Last annotation update)
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                                                                                                                    Artursson K., Gobl A., Lindersson M., "Molecular cloning of a gene encoding J. Interferon Res. 0:0-0(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00143; Interferon; 1. PRINTS; PR00266; INTERFERONAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q681Q4 PIG PRELIMINARY;
Q681Q4;
25-OCT-2004 (TEMBLEE]. 28,
25-OCT-2004 (TEMBLEE]. 28,
25-OCT-2004 (TEMBLEE]. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                             NUCLEOTIDE SEQUENCE.
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NCBI_TaxID=9823;
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NCBI_TaxID=9913;
                                                                                                                                                                                                                          BOVIN
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
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           Query Match
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                                                                                                                                                                                                                          <u>IFNB2</u>BO
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Matches
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                                                                                                                                                                                            EMLONIFAIFRODSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120
                                                                                                                                                          81
                                                                                                                                                22 MSYDVLRYQQRSSNLACQKLLEQLPGTPQYCLEDRMNFEVPEEIMQPPQFQREDAVLIIH
                                                                                                                                   1 MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
                                                                                                              Gaps
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Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Felidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-linked (GlcNAc. . .) (Potential).
                                                                                                              7
                                                                                        DB 2; Length 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (By similarity).
SUBUNIT: Monomer (By similarity).
SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Belongs to the alpha/beta interferon family.
                                                                                                                                                                                                                                      121 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN 166
                                                                                       Query Match
Best Local Similarity 62.0%; Pred. No. 8.9e-36;
Matches 103; Conservative 28; Mismatches 34; Indels
Pfam; PP00143; Interferon; 1.
PRINTS; PR00266; INTERFERONAB.
Prodom; PD000550; Interferon_abd; 1.
SMART; SM00076; IFabd; 1.
PROSITE; PS00252; INTERFERON_AB_D; 1.
Antiviral defense; Cytokine.
SEQUENCE 186 AA; 21950 MW; 79D70E53C3ADD6DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            By similarity.
25C359B1808AC862 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0266; INTERPERONAB.
ProDom; PD000550; Interferon abd; 1.
PROSITE; PS00252; INTERPERON A B D; 1.
Antiviral defense; Cytokine; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interferon beta.
                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-WAY-2005 (Rel. 47, Last annotation update)
Interferon beta precursor (IFN-beta).
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                                                                                                                                                                                                                                                                                                          186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22188 MW;
                                                                                                                                                                                                                                                                                                                                                                           Name=IFNB1; Synonyms=IFNB;
Felis silvestris catus (Cat).
                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101
131
136
136
52
186 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Felinae, Felis.
NCBI_TaxID=9685;
                                                                                                                                                                                                                                                                                               IFNB FELCA
ID IFNB FELCA
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CARBOHYD
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                           61 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120
                                                                                                                                                                                                                                          82 EMFQKIFNIFSRSTSSTGWNETTVENLLATLHWQKEHLETILEEIMEEENFTWDN-TTLL 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82
                                                                                                                                   22 VSYKLLGFQLRSSSLBCQELLVNLNRTSKYCLKDRMNFEVPEBIKKSQRFQKEEAILVIN 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSYNLLGFLORSSNFOCOKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aborechnology (N.Y.) 2:458-464(1984).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000471; Interferon abd.
PANTHER; PTHRIL691; Interferon abd; 1.
PFEM; PF00143; Interferon; 1.
PRON266; INTERFERONAB.
PROSUM; PD000550; INTERFERONAB.
PROSUTE; PS00222; INTERFERONA B D; 1.
Antiviral defense; Cytokine; Glycoprotein; Multigene family; Signal.
                                                     Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=IFNB2;
Doss taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
Leung D.W., Capon D.J., Goeddel D.V.;
"The structure and bacterial expression of three distinct bovine interferon-beta genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-linked (GlcNAc. . .) (Potential)
N-linked (GlcNAc. . .) (Potential)
                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 186;
Length 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBUNIT: Monomer.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the alpha/beta interferon family.
                                                                                                                                                                                                                                                                                                                                                    HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.4%; Score 492.5; DB 1; Lengua
57.9%; Pred. No. 2.4e-32;
Winmarrhes 38; Indels
                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D9F257C6E3250480 CRC64;
  59.8%; Score 522.5; DB 1;
61.4%; Pred. No. 8.5e-35;
iive 27; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interferon beta-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M15478; AAA30580.1; -; Genomic_DNA PIR; A01840; IVBOB2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22319 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interferon beta-2 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                           Best Local Similarity 61.4
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 1
52 1
186 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P01574; 1AU1
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Manager of the Comment

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IFNB1 BOVIN
ID IFNB1 BOVIN
AC P01578;
DT 21-JUL-1986 (;
DT 21-JUL-1986 (;
                              FNB3 BOVIN P01577;
                                                                                                  Name=IFNB3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                         removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11
BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                       I FNB3
                                   8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                     This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83 MLQOIFNILTRDFSSTGWSETIIEDLLEELYEQMAHLEPIQKEIMQKQNSTMGD-TTVLH 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120
MLONIFAIFRODSSSTGWNETIVENLLANVYHOINHLKTVLEEKLEKEDFTRGKLMSSLH 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
                                                                                                                                                                                                                                                                      MEDLINE=87053170; PubMed=3022999; Himmler A., Hauptmann R., Adolf G.R., Swetly P.; Molecular cloning and expression in Escherichia coli of equine type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                   DNA 5:345-356(1986).
-!- FUNCTION: Has antiviral, antibacterial and anticancer activities
                                                                                                                                                                                                               Eŭkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Perissodactyla, Equidae, Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-linked (GlcNAc. . .) (Potential)
N-linked (GlcNAc. . .) (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.8%; Score 487.5; DB 1; Length 186; 59.0%; Pred. No. 6.1e-32; ive 27; Mismatches 40; Indels 1.
                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Belongs to the alpha/beta interferon family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN 166
                                                       By similarity.
AE9F3ADFC006EE6C CRC64;
                                            122 LKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0266; INTERFERONAB.
ProDom; PD000550; Interferon abd; 1.
PROSITE; PS00252; INTERFERON A B D: 1.
Antiviral defense; Cytokine; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interferon beta.
                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                         ¥.
                                                                                                                          186
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M14546; AAA310954.1; -; Genomic_DNA.PIR; G24912; IVHOBI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; PO1574; 1AU1.
InterPror, IPRO00411, Interferon_abd.
PANTHER; PTHR11691; Interferon_abd; 1.
Pfam; PF00143; Interferon; 1.
                                                                                                                                                                              Interferon beta precursor (IFN-beta)
Name=IFNB1; Synonyms=IFNB;
Equus caballus (Horse).
                                                                                                                                                                                                                                                                                                                                          -!- SUBUNIT: Monomer.-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161 B
21882 MW;
                                                                                                                                                                      Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98; Conservative
                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186
                                                                                                                                                         13-AUG-1987 (Rel. 05,
10-MAY-2005 (Rel. 47,
                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                       NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101
136
52
                                                                                                                         HORSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S:
Matches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                    removed.
                                                                                                                         IFNB_HO
P05012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                IFNB_HORSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83 MLQQIFNILTRDFSSTGWSETIIEDLLVELYGQMNRLQPIQKEIMQEQNFTWGD-TTVLH 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 SYSLLRPQORRSAEVCQKLLGQLHSTPQHCLEAKMDFQVPEEMNQAQOFRKEDAILVIYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 SYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              interferon-beta genes.";
Biocechology (N.Y.) 2:458-464(1984).
-!- FUNCTION: Has antiviral, antibacterial and anticancer activities.
-!- SUBUNIT: Monomer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0266; INTERFERONAB.
PRODOM; PD000550; INTERFERONAB.
PROSITE; PS00252; INTERFERON A B D; 1.
Antiviral defense; Cytokine; Glycoprotein; Multigene family; Signal.
                                                                                                                                                                             Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                Leung D.W., Capon D.J., Goeddel D.V.;
"The structure and bacterial expression of three distinct bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GlcNAc. . .) (Potential) (GlcNAc. . .) (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: Belongs to the alpha/beta interferon family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 LKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1D10111EBEE1A65D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interferon beta-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-linked (GlcNAc.
N-linked (GlcNAc.
Probable.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.5%; Score 458.5; DB 1
53.3%; Pred. No. 1.4e-29;
iive 35; Mismatches 41
                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last annotation update)
Interferon beta-3 precursor.
186 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ą
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01, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M15479; AAA30581.1; -; Genomic_DNA.
PIR; A01841; IVBOB3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP, PO1574; 1AU1.
InterPro, IRR00041; Interferon_abd.
PANTHER; PTHR11691; Interferon_abd; 1.
Pfam; PF00143; Interferon; 1.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                       Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22060 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173
52
186 AA;
                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                          NCBI_TaxID=9913;
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation update)
10-MAM-2005 (Rel. 47, Last annotation update)
10-MAM-2005 (Rel. 47, Last annotation update)
10-MAM-21fabl, Synonyms=1fb, Ifab;
10-MAM-21fabl, Synonyms=1fb, Ifabl, Ifab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYNLLGFLORSSNFQCQKLLMQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Gaps
                                                                                                                                                                       PRINTS; PR00266; INTERFERONAB.
Probom; PR000550; Interferon abd; 1.
PROSITE; PS00252; INTERFERON A B D; 1.
Antiviral defense; Cytokine; Glycoprotein; Multigene family; Signal.
                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-linked (GlcNAc. .) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.4%; Score 440.5; DB 1; Length 186; 51.5%; Pred. No. 4.2e-28; ive 36; Mismatches 43; Indels 1;
                                                                                                                                                                                                                                                            -!- SUBUNIT: Monomer.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the alpha/beta interferon family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22195 MW; F9060C07EA415B9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interferon beta-1.
10-MAY-2005 (Rel. 47, Last annotation update)
Interferon beta-1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 AA
                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M15477; AAA30579.1; -; Genomic_DNA.
PIR; A01842; IVBOB1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000471; Interferon abd.
PANTHER; PTHR11691; Interferon abd; 1.
Pfam; PF00143; Interferon; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probable.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
                                                                                                       Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 51.5%;
nes 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131
173
161
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                                                       Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 1
173 1
52 1
186 AA;
                                                                                                                                                          NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P01574; 1AU1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                          NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IFNB MOUSE
P01575;
                                       Name=IFNB1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ~
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                  removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IFNB_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.75 ANGSTROMS).
Senda T., Mateuda S., Kurihara H., Nakamura K.T., Kawano G.,
Shimizu H., Mizuno H., Mitsui Y.;
Three-dimensional structure of recombinant murine interferon-beta.";
Proc. Jpn. Acad., B, Phys. Biol. Sci. 66:77-80(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Three-dimensional crystal structure of recombinant murine interferon-
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MEDLINE=9662813; PubMed=7473712;
Senda T., Saitoh S.-I., Mitsui Y.;
"Refined crystal structure of recombinant murine interferon-beta at
MEDLINE=83265757; PubMed=6688252;
Higashi Y., Sokawa Y., Watanabe Y., Kawade Y., Ohno S., Takaoka C.,
Taniguchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIJNE=89125582; PubWed=3221389; Vodjdani G., Coulombel C., Doly J.; Vodjdani G., Coulombel C., Doly J.; Structure and characterization of a murine chromosomal fragment containing the interferon beta gene."; J. Mol. Biol. 204:221-231(1988).
                                                                                                                        "Structure and expression of a cloned cDNA for mouse interferon-

    -!- SIMILARITY: Belongs to the alpha/beta interferon family.

                                                                                                                                                                                                                                                                   NUCLECTIDE SEQUENCE.
MEDIINE=89263735; PubMed=2726460;
MEDIINE=89263735; PubMed=2726460;
MEDIINE=89263735; PubMed=2726460;
MEDIINE=8926376 T.;
Nuclectide sequence of the mouse interferon-beta gene.";
Nucleic Acids Res. 17:3291-3291(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92371425; PubMed=1505514;
Senda T., Shimazu T., Matsuda S., Kawano G., Shimizu H.,
Nakamura K.T., Mitsui Y.;
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PDB; 1WU3; X-ray; 1=22-182.
PDB; 1HF; Model; @=24-182.
Ensembl; ENSMUSG0000048806; Mus musculus.
MGI; MGI:107657; Ifhb..
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0005125; F:cytokine activity; IDA.
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EMBL; X14455; CAA32625.1; -; Genomic_DNA.
EMBL; X14029; CAA32190.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
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Eur. J. Biochem. 173:311-316(1988)
                                                                                                                                                                                                   Biol. Chem. 258:9522-9529(1983)
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PDB; 11FA; X-ray; @
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
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MEDLINE=97271387; PubMed=9126338; DOI=10.1006/bbrc.1997.6359;
Yokoyama S., Ohishi N., Shamoto M., Watenabe Y., Yagi K.;
Isolation and expression of rat interferon beta gene and growth-inhibitory effect of its expression on rat glioma cells.";
Biochem. Biophys. Res. Commun. 232:698-701(1997).
            Interpro; IPR000471; Interferon abd.
PANTHER; PTHR11691; Interferon abd; 1.
Pfam; PR00143; Interferon; 1.
PRINTS; PR00266; INTERFERONAB.
PRODOM; PD000550; INTERFERONAB.
PROSITE; PS00252; INTERFERON_A B D; 1.
3D-structure; Antiviral defense; Cytokine; Glycoprotein; Signal.
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 GO:0042830; P:defense response to pathogenic bacteria; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.2%; Score 342.5; DB 1; Length 182; 46.4%; Pred. No. 4.1e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22127 MW; 8C4C32947FD1B917 CRC64;
                                                                                                                                                Interferon beta.
N-linked (GlCNAc. .).
N-linked (GlCNAc. .).
N-linked (GlCNAc. .).
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01-NOV-1997 (Rel. 35, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.4%; Pred. No. 4.1e-
tive 27; Mismatches
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Name=1fnb1, Synonyms=1fnb;
Rattus norvegicus (Rat).
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Best Local Similarity 46...
Local Similarity 46...
The Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 IDYKOLOFROSTSIRTCOKLLROLNGRLN--LSYRTDFKIPMEVMHPSOMEKSYTAFAIQ
FUNCTION: Has antiviral, antibacterial and anticancer activities. SUBUNIT: Monomer (By similarity). SUBCELLULAR LOCATION: Secreted.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=15183033, DOI=10.1016/j.dci.2004.02.002;
PubMed=15183031, DOI=10.1016/j.dci.2004.02.002;
Harrison G.A., McNicol K.A., Deane E.M.;
Literferon alpha/beta genes from a marsupial, Macropus eugenii.",
Dev. Comp. Immunol. 28:927-940(2004).
I- SUBCELLULAR LOCATION: Secreted (By similarity).
EMBL; AX165862; AAO37658.1; -; Genomic_DNA.
HSSP; PO1574; 1AU1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Metatheria, Diprotodontia, Macropodidae, Macropus.
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                                                                        -!- PTM: This beta interferon does not have a disulfide bond -!- SIMILARITY: Belongs to the alpha/beta interferon family.
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                      EMBL; D87919; BAA13502.1; -; Genomic_DNA.
PIR; JC5424; JC5424.
HSSP; P01574; JAU1.
SMS; P70495; 22-184.
Ensembl; ENSRNGG0000006268; Rattus norvegicus.
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Q7YRX6;
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les 76; Conserv
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GO: 0005526; F: hematopoietin/interferon-class (D200-domain. .; IEA.
GO; GO: 0005522; P: defense response; IEA.
InterPro; IRR000471; Interferon_abd.
Pfam; PF00143; Interferon; 1.
PRINTS; PR002650; INTERFERONAB.
PRODOM; PD000550; INTERFERONAB.
SWART; SW00076; IFAbd; 1.
PROSITE; PS00252; INTERFERON A_B_D; UNKNOWN_1.
GO; GO:0005126; F:hematopoietin/interferon-class (D200-domain. .; IEA. GO; GO:0006952; P:defense response; IEA. InterPro; IRR000471; Interferon_abd. Pfam; PF00149; INTERFERONAB. PRODOM; PRO0266; INTERFERONAB. PRODOM; PRO0566; INTERFERONAB. PRODOM; PB000550; Interferon_abd; 1. PROSITE; PS00252; INTERFERON_ABD; 1. Antivital defense; Cytokine. SEQUENCE 183 AA; 21215 MW; E20859376477B5F9 CRC64;
                                                                                                                                                                                                                                                                                                  24 YDSLRFHQRRTNRRSLSLLKEMIGEIHPECLREGMDFKIPQEIVQPKQCQKENATWVIHE
                                                                                                                                                                                                                                                                            3 YNLLGFLQRSSNFQCQKLLWQLNGRLE-YCLKDRMNFDIPEEIKQLQQFQKEDAALTIYE
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Harrison G.A., McNicol K.A., Deane E.M.;
Type I interferon genes from the egg-laying mammal, Tachyglossus aculeatus (short-beaked cchidna). ";
Immunol. Cell Biol. 82:112-118(2004).
EMBL; AY194920; AAP34279.1; -; Genomic_DNA.
HSSP; P01574; IAUI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tachyglossus aculeatus (Australian echidna).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Monotremata, Tachyglossidae, Tachyglossus.
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                                                                                                                                                                                                Query Match 35.2%; Score 30%; DB 2; Length 183; Best Local Similarity 42.4%; Pred. No. 2.7e-17; Matches 70; Conservative 31; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         122 LKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                22496 MW; 00A7FAC603EA58E5 CRC64;
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Last sequence update)
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SEQUENCE 187 AA; 22496 M
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QEXZW6;
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Best Local Similarity
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Search completed: December 21, 2005, 14:21:43 Job time : 229 secs

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RESULT 1
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                                                                     December 21, 2005, 13:55:56; Search time 187 Seconds (without alignments) 390.037 Million cell updates/sec
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Aaw81774
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                                                                                                                                                                                                              2443163 seqs, 439378781 residues
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GenCore version
Copyright (c) 1993 - 2005
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Gapop 10.0 , Gapext 0.5
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geneseqp2001s:*
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r n	Adh21850 Human mod Adh21357 Human IFN Adh21851 Human mod Adh21356 Human IFN	Human Human Human	Human Human Human Human	Ad190995 Human int Ad197822 Human int Ad188862 Human cyt Ad188863 Human cyt	Ad189974 Human cyt Adn10814 Human int Ad043932 Amino aci
7 ADF17215 7 ADF70842 7 ADG75820	7 ADH21850 7 ADH21357 7 ADH21851 7 ADH21356	7 ADH21368 7 ADH21370 7 ADH21852	3 ADH78593 3 ADJ56127 3 ADJ50897 8 ADL71379	8 ADL90995 8 ADL97822 8 ADL88862 8 ADL88863	
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ALIGNMENTS

Sequence of interferon (HuIFN) -beta-1 encoded by plasmid pDM101/trp/beta Hybrid interferon; antiviral; therapy; cancer; tumour AAP30219 standard; protein; 166 AA 83US-00340782. 83US-00463574. 85US-00755265. 82US-00340782 (revised)
(first entry) CORP. (CETU) CETUS (CETU) CETUS 19-JAN-1982; 03-FEB-1983; 15-JUL-1985; Homo sapiens 19-JAN-1982; 25-MAR-2003 25-MAY-1992 WO8302461-A 21-JUL-1983 AAP30219; AAP30219

Creasey AA; Mark DF,

WPI; 1983-723186/30. N-PSDB; AAN30152 $\mathtt{Multi:class}$ hybrid interferon poly:peptide(s) - with restricted antiviral and cell growth regulatory activities.

Example, Fig 5; 61pp; English

The inventors claim a multiclass hybrid interferon polypeptide and a DNA unit having a nucleotide sequence which encodes it. Pref. the AA sequence consists of alpha and beta interferons. Pref. IT is (i) the 1-73 AA seq. of HuFN-alpha-1 (and IF2 is the 74-166 AA seq. of HuFN-beta-1) (see AAN30155, AAP30222); or (ii) the 1-41 AA seq. of HuFN-beta-1) (see AIN30156, AAP30227).

Alternativeley IP1 is the amino terminal end of a beta-IF and IF2 is the anaboxy terminal of an alpha-IF (sep. the 1-73 seq. of HuFN-beta-1 and

Human Human ö

Gaps

0

Indels

Length 166;

100.0%; Score 874; DB 1; 100.0%; Pred. No. 2.1e-69;

100.0%;

0; Mismatches

120

9

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61 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLBEKLEKEDFTRGKLMSSL 120
                                                                                          EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL
                                                                          1 MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
                                                                                                                                                                                           HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN 166
                                        Best Local Similarity 100.
Matches 166; Conservative
                                       Similarity
 Sequence 166 AA;
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09-DEC-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The inventors claim a process for the prodn. of heterologous polypeptide by transformed bacteria. The pref. promoter-operator is trp which controls expression of structural genes encoding polypeptides of a synthetic pathway forming tryptophan, esp. at a concn. of 5.3T mg/l (Tepredetermined turbidity value measured at 680nm, esp. 10-100). The transformed bacteria are esp. E.coli contg. the plasmid p-beta-1-trp. Example 1 concerns the construction of plasmid p-beta-1-trp direct expression of IFN-beta under the control of trp promoter-operator. (Updated on 03-OCT-2002 to add missing OS field.)
                                                                                                                                                                                                                       120
the 74-167 seq. of HuIFN-alpha-1 resp.) (see AAN30156, AAP30223). In the examples plasmids pGW5 and pDM101/trs/beta-1 and p-alpha-61A were used (see AAN30151, AAN30152, AAN30157). HinfI was used to digest the DNA sequence in the region of significant handicaps (see AAN30153, AAN30154, AAN30158, AAN30159), and the restriction fragments were ligated to form hybrid DNA. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                      61 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLBKEBFTRGKLMSSL 120
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                                                                                                                                                                     1 MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence encoded by the sequence between the EcoRI site and the XhoII
                                                                                                                                             Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polypeptide, esp. interferon, prodn. by transformed bacteria in presence of a repressor which is consumed during growth.
                                                                                                                  Length 166;
                                                                                                                                                                                                                                                                          HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN 166
                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                         HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
                                                                                                                 100.0%; Score 874; DB 1;
100.0%; Pred. No. 2.1e-69;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                   AAP50262 standard; protein; 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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Best Local Similarity 100.
Matches 166; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          site of p-beta-l-trp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Konrad MW, Mark DF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CETUS CORP.
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                                                                                           Sequence 166 AA;
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20-NOV-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence encodes a synthetic interferon-beta which has increased biological activity compared to natural IRN-beta, and which is more effective in the treatment of viral or neoplastic diseases, or immunosuppressed or immunodeficient conditions. (Updated on 25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New modified beta-interferon(s) - useful as antiviral, anti-neoplastic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                    Protein sequence encoding synthetic interferon-beta gene
                                                                                                                                                                                                                Interferon-beta; virucide; antitumor; immunostimulant.
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Pred. No. 2.1e-69;
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AAP50279 standard; protein; 166 AA
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100.0%; Pr
tive 0;
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es 166; Conserv
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Modified peptide has residues susceptable to chloramine T and peroxide oxidation replaced with conservative AAs. Mutein is thus resistant to oxidistation. Other proteins which may be similarly rendered resistant include tissue plasminogen activator, colony stimulating factor and human growth factor. (Updated on 03-OCT-2002 to add missing OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMLONIFAIFRODSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oxidn. resistant mutein(s) - prepd. by replacing oxidn.-susceptible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or absent"
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                                                                                                                                                                                                                                                                                               IL-2; IFN-Beta; colony stimulating factor; CSF-1; tPA; hGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note≈ "May be N-terminal truncated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note= "May be any conservative AA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "May be any conservative AA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "May be any conservative
                                                                                                                                                                                                                                                 Oxidation resistant mutein of Interferon-Beta
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                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                      AAP61071 standard; protein; 166
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85US-00810656.
86US-00893186.
86AU-00064846.
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                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1986-239075/37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 166 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
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                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JAN-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JAN-1985;
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                                                                                                                                                                 03-OCT-2002
28-MAY-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                             AAP61071;
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The inventors claim an interferon conjugate wherein a C-terminal of the region exhibiting biological activities of interferon-beta has been linked to an N-terminal of the region exhibiting biological activities of interferon-gamma. The antiviral activity of the conjugate was tested using FL cells-sindbis virus system according to the CPE 50 inhibition method. Antiviral activity ranged from 200 U/ml to 18500 U/ml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conjugates of interferon(s)-beta and-gamma - useful as antivirals and anti-cell proliferatives with broader spectrum of activity and obtd. economically by recombinant DNA procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
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100.0%; Score 874; DB 1; Length 166;
Best Local Similarity 100.0%; Pred. No. 2.1e-69;
Matches 166; Conservative 0; Mismatches 0; Indels (
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                        166
121 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN
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                                                                                                                                                                                            Antiviral; antiproliferative agent
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                                                                                        AAP70296 standard; protein; 166
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                                                                                                                                                                                                                                                                                                                        86JP-00054650.
86JP-00308693.
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                                                                                                                                                                    interferon-beta
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                                                                                                                                                                                                                                                                                                                                                                                         Kawano G,
                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1987-258309/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 166 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JAN-1999
                                                                                                                                                                                                                                                                                                10-MAR-1987;
                                                                                                                                                                                                                                                                                                                                       26-DEC-1986;
                                                                                                                                                                                                                                                                                                                          14-MAR-1986;
                                                                                                                                                                   Sequence of
                                                                                                                                            07-JUN-1991
                                                                                                                                                                                                                                                                       16-SEP-1987
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                                                                                                                   AAP70296;
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                                                                                                                                                                                                                                                                             New mutated recombinant human interferon-beta protein contains hydroxylic amino acid substitutions to improve water solubility - used e.g. in in vitro screening assays, to measure interferon levels and to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120
                                                                                                                                                                                                                                                                                                                                                               This sequence represents a native human recombinant interferon-beta protein which is mutated into an amino acid having at least one hydroxy group substituted for at least one of LeuS, Phe8, Phe15, Leu47, Phe50, Leu106, Phe111, Leu116, Leu120 and Phe156. Such mutants can be used in medicaments e.g. for treating multiple sclerosis, for in vitro screening assays and for measurement of interferon levels. The mutated protein is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human; amniotic membrane; beta-interferon; IFN; IFN type 1; growth; cellular differentiation; immunoregulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                             more water-soluble than recombinant wild-type human interferon-beta
                                 Interferon-Beta; variant; human; medicament; treatment; screening;
multiple sclerosis; measurement; water soluble.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human amniotic membrane beta interferon (IFN) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 874; DB 2;
100.0%; Pred. No. 2.1e-69;
iive 0; Mismatches 0;
                                                                                                                                                                                                     (FRAU ) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN
                                                                                                                                                                                                                              Waschuetza G;
          Human native interferon-beta protein.
                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 1; 18pp; German.
                                                                                                                                                                                                                              Otto B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADR83685 standard; protein; 166
                                                                                                                                                  97DE-01017864
                                                                                                                                                                           97DE-01017864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166; Conservative
                                                                                                                                                                                                                              Schneider-Fresenius C,
                                                                                                                                                                                                                                                      WPI; 1998-569784/49
                                                                                                                                                                                                                                                                                                                     multiple sclerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 166 AA;
                                                                                               DE19717864-A1
                                                                          Homo sapiens
                                                                                                                                                  23-APR-1997;
                                                                                                                                                                             23-APR-1997;
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                                                                                                                           29-OCT-1998
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Ното варіепв

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                                                                                                                                                                                                                                                  Production of recombinant human amniotic membrane interferon comprises cell cultivation for infection with Sendai virus, production of mRNA, RNA fractionation, dissolution.
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                                                                                                                                                                                                                                                                                                                                                                                     This invention relates to a novel method for producing human amniotic membrane beta-interferon (IFN) protein (also identified as beta-IFN type 1). Specifically, it refers to production of the recombinant protein through genetic engineering techniques that can be used in medicine, weterinary science and research. In particular, the human amniotic membrane beta-IFN protein is important in the regulation of growth and cellular differentiation and the immunoregulation of biological systems. The present invention describes the process of cDNA amplification, coloning and transforming competent bacteria then selecting those clones that express the beta-IFN protein, which is then extracted and purified. This polypeptide sequence is the human beta-IFN protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            °,
                                                                                                                                Peregrino Ferreira PC, Rolland Golgher R, Geessien Kroon E;
Bonjardim CA, Fiorini De Carvalho A, Rodrigues Dos Santos J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 874; DB 3; 100.0%; Pred. No. 2.1e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 1; 16pp; Portuguese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB49356 standard; protein; 166 AA
                                                                                          FEDERAL MINAS GERAIS
  97BR-00010827.
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                                               97BR-00010827.
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                                                                                                                                                                                                       WPI; 2000-423633/37.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200068387-A2
                                                                                          VINU (-IMYU)
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16-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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-beta related disorders such as multiple sclerosis.
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                                                                                                                                                                                                                                                                                                                                                           RESULT 10
AAE10346
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                                                                                                                                    beta) activity. These analogues are produced so that they are less than 97% identical to human IFN-beta. They are useful in the treatment of multiple sclerosis, cancer, particularly osteosarcoma, basal cell carcinoma, cervical dysplasia, glioma, acute myeloid leukaemia, multiple myeloma, Hodgkin's disease, melanoma, and renal, liver and breast cancers, vixal infections, including those caused by hepatisis viruses, herpes viruses and papilloma viruses, viral encephalitis, cytomegalovirus pneumonia and prophylaxis of rhinovirus, idiopathic pulmonary fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel interferon-beta activity (IbA) proteins which have greater etability than interferon-beta (IFN-beta) useful for the treatment of IFN
                                                                                                                                                                                                                                                                                                                                                              Novel interferon-beta activity (IbA) proteins which have greater stability than interferon-beta (IFN-beta) useful for the treatment of IFN-beta related disorders such as multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                    EMLONIFAIFRODSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120
                                                                                                                                                                                                                                                                                                                      1 MSYNLLGFLQRSSNPQCQKLLMQLNGRLEYCLKDRMNFDIPBEIKQLQQFQKEDAALTIY 60
                                                                                                                                                                                                                                                                                                           9
                                                                                                                             The present invention provides proteins which have interferon-beta (IFN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interferon-beta activity; multiple sclerosis; cancer; viral infection;
                                                                                                                                                                                                                                                                                                         1 MSYNLLGFLORSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEBIKQLQQFQKEDAALTIY
                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                Length 166;
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                                                                                                                                                                                                                                                                   100.0%; Score 874; DB 4; 100.0%; Pred. No. 2.1e-69;
                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                           Disclosure; Fig 1A; 109pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB49357 standard; protein; 166
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                                                                                                                                                                                                                            and inflammatory diseases
                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human INF-beta B-chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-007398/01.
                                                                                                                                                                                                                                                                              Local Similarity
     (XENC-) XENCOR INC
                                                                                                                                                                                                                                                Sequence 166 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (XENC-) XENCOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200068387-A2.
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                                                                                                                                                                                                                                                                     Query Match
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                                      The present invention provides proteins which have interferon-beta (IFN-beta) activity. These analogues are produced so that they are less than by a interfical to human IFN-beta. They are useful in the treatment of multiple sclerosis, cancer, particularly osteosarcoma, basal cell carcinoma, cervical dysplasia, glioma, acute myeloid leukaemia, multiple myeloma, Hodgkin's disease, melanoma, and renal, liver and breast cancers, viral infections, including those caused by hepatitis viruses, herpes viruses and papilloma viruses, viral encephalitis, cytomegalovirus promomonia, and prophylaxis of rhinovirus, idiopathic pulmonary fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLBEKLEKEDFTRGKLMSSL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSYNLLGFLQRSSNFQCQKLLMQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 874; DB 4;
100.0%; Pred. No. 2.1e-69;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "TSO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE10346 standard; protein; 166 AA
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07-NOV-2000; 2000US-0246089P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mature human beta-interferon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-FEB-2001; 2001EP-00103580
Example 1; Fig 1B; 109pp;
                                                                                                                                                                                                                                                                                                                                              and inflammatory diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SA
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoimmune disease.
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                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 166 AA;
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9; Page 15; 21pp; English

Claim

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The invention relates to use of nucleic acids expressing human beta-
interferon (INF-beta) for the treatment of immune diseases such as
demyelinating disease (e.g. sub-acute sclerosing panencephalomyelitis
(SSPE), metachromatic leukodystrophy, Guillain-Barre syndrome) and
autoimmune disease (e.g. multiple sclerosis). The expression of the beta-
interferon results in the improvement of the clinical status of the
treated mammal, thus avoiding the use of recombinant polypeptide. The
nucleic acid is therefore compatible with the quality of life of the
patients. The present sequence is mature human beta-interferon
                                                                                                                                                                                                                                                                                                                                                                                            61 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A conjugate exhibiting interferon beta activity useful for treating multiple sclerosis comprises a non-polypeptide group covalently attached to an interferon beta polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; interferon beta; antibody; multiple sclerosis; gene therapy; viral infection; viral hepatitis; cancer; breast cancer; inflammation; Crohn's disease; acute myeloid leukaemia; Hodgkin's disease; ulcerative colitis; immunodulation.
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                                                                                                                                                                                                                                                       100.0%; Score 874; DB 4;
100.0%; Pred. No. 2.1e-69;
ive 0; Mismatches 0;
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99DK-00001691.
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Best Local Similarity 100.
Matches 166; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human interferon beta.
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                                                                                                                                                                                                                       Sequence 166 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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AAU00038
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The sequence is Human interferon beta. Conjugates of the invention exhibiting interferon beta activity comprise at least one first non-polypeptide group covalently attached to an interferon beta polypeptide, the amino acid sequence of which differs from wild-type human interferon beta in at least one introduced and at least one removed amino acid group. The invention also concerns reducing the immunogenicity and/or increasing functional in vivo half-life and/or serum half-life of an interferon beta polypeptide comprising introducing an amino acid residue constituting an attachment group for a first non-polypeptide group interferon beta polypeptide comprising introducing an amino acid residue agroup and removing an amino acid residue constituting an attachment are set the protein that does not contain such a group and removing an amino acid residue constituting an attachment
                                                                                                                                                                                                                                                                                  group for a first non-polypeptide group and subjecting the modified peptide to conjugation with the non-polypeptide group. The conjugate and a cell culture expressing the mutated polypeptides are useful in the treatment of disease, especially multiple sclerosis, and for treating mammals having circulating antibodies against interferon beta la or lb. DNA encoding the mutated proteins may be used for gene therapy. The DNA and proteins can also be used to treat viral infections (e.g viral hepatitis), cancer (e.g. breast cancer), inflammation, Crohn's disease, acute myeloid leukaemia, Hodgkin's disease and ulcerative collitis and for immunomodulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
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100.0%; Pred. No. 2.1e-69;
ive 0; Mismatches 0;
Example 1; Page 99-100; 108pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human wild-type interferon (IFN) beta.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE11979 standard; protein; 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-MAR-2000; 2000DK-00000447.
20-MAR-2000; 2000US-0190844P.
25-AUG-2000; 2000WO-DK000471.
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nes 166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 166 AA;
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(MAXY-) MAXYGEN APS

Rasmussen PB;

Bornaes C,

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Indels

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Length 166;

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The present invention relates to novel dispersions of a conjugate comprising at least one non-polypeptide moiety covalently attached to a polypeptide variant, wherein the amino acid sequence of the polypeptide variant differs from that of the corresponding wild-type human polypeptide from the corresponding wild-type human polypeptide group has been introduced and/or removed. The wild-type human polypeptide group has been introduced and/or removed. The wild-type human polypeptide is selected from the group consisting of interferon-gamma (IFNG), interferon-beta, interferon alpha, follicle stimulating hormone, (FSH), interferon-beta, interferon alpha, follicle stimulating factor (G-CSF). The dispersion is used for the preparation of a medicament for pulmonary and/or circulatory administration. The present sequence is human wild type interferon (IFN) beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; interferon-beta; IFN-epsilon; cytostatic; immunosuppressive; virucide; gene therapy; autoimmune disease; lymphoproliferative disorder; cancer; tumour; B-cell lymphoma; lymphatic leukaemia; immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120
                                                                       Dispersions of particles for administration to the lung and circulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 874; DB 4; 100.0%; Pred. No. 2.1e-69;
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                                                                                        system by inhalation, e.g. from a nebulizer.
                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                          Claim 22; Page 136; 139pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE16797 standard; protein; 166
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99US-0118578P.
99US-0142766P.
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Les 166; Conservative
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                                             WPI; 2001-616274/71
                                                                                                                                                                                                                                                                                                                                                                       Sequence 166 AA;
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08-JUL-1999;
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             Hansen CK
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                                                                                                                 The invention relates to an isolated nucleic acid molecule encoding a murine interferon epsilon (IFN-epsilon, Zifne) polypeptide. IFN-epsilon DNA is useful for producing IFN-epsilon polypeptides which is useful for treating autoimmune diseases, cancers, tumours and lymphoproliferative disorders including B-cell lymphoma, chronic lymphatic leukaemia and acute lymphatic leukaemia. IFN-epsilon protein is useful for the enhancement of immune response against infectious agents, e.g. virus. IFN epsilon DNA is useful in gene therapy. The present sequence is human interferon (IFN)-beta protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BMLQNIFALFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120
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         acid molecules encoding interferon epsilon polypeptides useful ating certain autoimmune diseases, cancers and for the enhancement
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100.0%; Pred. No. 2.1e-69;
ive 0; Mismatches 0;
                                   for treating certain autoimmune diseases, car
of immune response against infectious agents.
                                                                                        Disclosure; Fig 1; 59pp; English
                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
nes 166; Conservative
                                                                                                                                                                                                                                                                                                                     Sequence 166 AA;
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Human, interferon beta, INFbeta, non-immunogenic, T-cell epitope, major histocompatibility complex, MHC class II ligand, MHC allotype, reduced immunogenicity. Human interferon beta (INFbeta) wild-type protein. Ą ABG97960 standard; protein; 166 (first entry) 07-JAN-2003 ABG97960; ABG97960

15-MAR-2002; 2002WO-EP002925 15-MAR-2001; 2001EP-00106539 (MERE) MERCK PATENT GMBH. WO200274783-A2. Homo sapiens. 26-SEP-2002

New modified molecule with the biological activity of human interferon (INF) beta that is non-immunogenic or less immunogenic than any non-modified molecule, useful for vaccination to reduce immunogenicity to INF WPI; 2002-750532/81 beta in vivo.

Baker M;

Watkins J,

Jones T,

Carter G,

Carr FJ,

1. ...

Disclosure; Page 5; 60pp; English

polypeptides that are substantially non-immunogenic or less immunogenic than any non-modified molecule having the same biological activity when sued in vivo. The modified molecule is obtained by altering or used in vivo. The modified molecule is obtained by altering or used in vivo. The modifications involve (a) removing one or more T-cell epitopes derived from the wild-type molecule and being major is obtained by altering or histocompatibility complex (MHC) class II ligands or peptides sequences that show the ability to stimulate or bind T-cells via presentation on bind peptides derived from the molecule. The modified polypeptides are useful in manufacturing INPbeta with reduced immunogenicity than any non-modified molecule with the same or acceptably reduced degree of modified molecule with the same or acceptably reduced degree of biological activity when used in vivo. The polypeptides are also useful for the vaccination of patients to reduce immunogenicity to INFbeta in vivo. The present sequence represents the wild-type human INFbeta protein EMLQNIFAIFRQDSSSTGWNETIVENLIANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120 invention relates to modified human interferon beta (INFbeta) 1 MSYNLIGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY Length 166; HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN 166 HIKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN 166 Indels 100.0%; Score 874; DB 5; 100.0%; Pred. No. 2.1e-69; ive 0; Mismatches 0; Wild-type human interferon beta protein. AAO26338 standard; protein; 166 AA 26-FEB-2002; 2002WO-DK000128. 16-JAN-2003 (first entry) Matches 166; Conservative Local Similarity Sequence 166 AA WO200274806-A2 Homo sapiens 26-SEP-2002 AA026338; 61 61 121 121 Query Match AA026338 ઠે g ò g ò 셤

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Neuroprotective, cytostatic; virucide, glycosylated variant; IFNB; interferon betea; glycosylation site; multiple sclerosis; cancer; breast; bladder cancer; herpes zoster; viral hepatitis; gene therapy; wild-type human interferon beta protein.
                                                                                                                                                                                                                                                                                          Pedersen AH;
                                                                                                                                                                                                                                                                                          Rasmussen G,
                                                                                                                                                                                                    27-FEB-2001; 2001DK-00000323.
                                                                                                                                                                                                             01-MAR-2001; 2001DK-00000333.
29-JUN-2001; 2001DK-00001040.
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21-DEC-2001; 2001DK-00001954.
                                                                                                                                                                                                                                                   2002DK-00000257
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                                                                                                                                                                                                                                                                                          Rasmussen PB, Drustrup
                                                                                                                                                                                                                                                                       (MAXY-) MAXYGEN APS
                                                                                                                                                                                                                                                   19-FEB-2002;
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WPI; 2002-750536/81. N-PSDB; AAL53464.

The invention relates to a glycosylated variant of a parent interferon beta (IFNB) polypeptide comprising at least one in vivo glycosylation site, where an amino acid residue of the parent polypeptide located close to the glycosylation site has been modified to obtain the variant polypeptide having an increased glycosylation as compared to the parent polypeptide. The variant, conjugate or composition, is useful in the treatment of, or in the manufacture of a treatment of diseases, in particular multiple sclerosis. The variant may also be used in treating cancer (e.g. breast or bladder cancer) or viral infections (e.g. herpes coster, viral hepatitis). The polymucleotide of the invention can be used in gene therapy. This sequence represents the wild-type human interferon beta protein of the invention ö EMIQNIFALFRODSSSTGWNETIVENLLANVYHOINHLKTVLEEKLEKEDFTRGKLMSSL 120 61 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLBEKLEKEDFTRGKLMSSL 120 9 9 1 MSYNLLGFLQRSSNPQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY 1 MSYNLLGFLORSSNFOCOKLLWOLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY Gaps New glycosylated variant of interferon-beta polypeptide, useful for treating multiple sclerosis, cancer or viral infections, comprises increased glycosylation activity compared to the parent polypeptide. ; 0 Length 166; HIKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN 166 0; Indels 100.0%; Score 874; DB 5; 100.0%; Pred. No. 2.1e-69; 0; Mismatches Claim 7; Page 100; 100pp; English. 166; Conservative Similarity Sequence 166 AA; Query Match Best Local 8 121 Matches ð d 셤 ઠ 8

> 9 9

Gaps ;

Search completed: December 21, 2005, 14:17:06 Job time : 190 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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using sw model protein search, OM protein

Run on:

December 21, 2005, 14:09:41; Search time 38 Seconds (without alignments) 420.315 Million cell updates/sec

US-10-084-706-2 Title: Perfect

1 MSYNLLGFLQRSSNFQCQKL.....RVEILRNFYFINRLTGYLRN 166 score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_80:* 1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description						beta			interferon alpha-1				interferon alpha-I			æ		trophoblast prote	u						interferon alpha-5	๙		ro -	trophoblast protei
COLUMNIA	Ü	IVHUB1	IVBOB2	IVHOBI	IVBOB3	IVBOB1	IVMSB	JC5424	IVH022	IVHO21	IVHOA1	IVHOA3	IVHOA4	IVHU16	137584	IVHOA2	IVBOII	A61578	A61455	I78570	IVHUII	I VHUA2	IVHU4B	F25843	IVHUAO	IVHUA7	153102	JS0204	152347	147068
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	Length	187	186	186	186	186	182	184	195	195	184	184	184	189	189	184	195	172	195	165	195	188	189	167	189	8	189	195	189	195
٠	Query Match	100.0	56.4	55.8	52.5	50.4	39.5	38.4	33.1	30.7	30.2	30.2	30.2	29.8	29.8	29.7	29.5	29.5	29.5	29.1	29.1	29.0	29.0	28.8	28.8		28.8	28.7		28.5
	Score	874	492.5	487.5	458.5	440.5	342.5	335.5	289	268	264	264	264	260.5	260.5	260	257.5	255.5	255.5	254.5	254	253.5			251.5	251.5			249.5	249.5
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trophoblast protei interferon alpha-1	interferon alpha-I	interferon-alpha -	interferon, tropho	interferon alpha-I	interferon type I	interferon alpha -	interferon-omega45	interferon precurs	trophoblast interf	trophoblast interf	trophoblast protei	interferon alpha -	interferon-omega20	interferon-omega44
147097 IVHUA9	IVHU14	156314	A53746	A61403	S70011	146398	146974	151970	S23751	A39505	147066	146397	146975	146972
77	Н	~	~	7	7	~	~	N	N	~	~	~	7	7
195	189	176	195	195	195	195	195	189	195	195	195	195	195	195
28.5	28.4	28.3	28.3	28.3	28.3	28.3	28.3	28.2	28.2	28.2	28.1	28.0	28.0	28.0
249.5	248	247.5	247	247	247	247	247	246.5	246.5	246.5	245.5	245	245	245

ALIGNMENTS

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interferon beta-1 precursor [validated] - human interferon beta-1 precursor [validated] - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text change 09-Jul-2004
C;Accession: A93721; A93887; Ā91468; A93225; A93706; A93700; A93269; S04479; I56315; A018 R;Lawn, R.M.; Adelman, J.; Franke, A.E.; Houck, C.M.; Gross, M.; Najarian, R.; Goeddel, I Nucleic Aindan fibroblast interferon gene lacks introns.
A;Title: Human fibroblast interferon gene lacks introns.
A;Reference number: A93721; MUID:81198952; PMID:6164984

A;Accession: A93721
A;Molecule type: DNA
A;Residues: 1-187 <LAM>
A;Cross-references: UNIPROT:P01574; UNIPARC:UP1000004775D; GB:V00535; NID:g32639; PIDN:CF
B;Ohno, S.; Taniguchi, T.
Proc. Natl. Acad. Sci. U.S.A. 78, 5305-5309; 1981
A;Title: Structure of a chromosomal gene for human interferon beta.
A;Reference number: A93887
A;Accession: A93887

A Molecule type: DNA A;Residues: 1-187 -06NA A;Cross-references: UNIPARC:UPI000004775D R;Taniguchi, T.; Ohno, S.; Fujii-Kuriyama, Y.; Muramatsu, M. Gene 10, 11-15, 1380 A;Title: The nucleocide sequence of human fibroblast interferon cDNA. A;Reference number: A91468; MUID:81005095; PMID:6157601

A; Accession: A91468

A;Molecule type: mRNA A;Reaidues: 1-187 <TAN> A;Cross-references: UNIPARC:UDI000004775D; GB:V00546; NID:g32735; PIDN:CAA23807.1; PID:g. K;Derynck, R.; Content, J.; DeClercq, E.; Volckaert, G.; Tavernier, J.; Devos, R.; Fiers, Nature 285, 542-547, 1980 A;Title: Isolation and structure of a human fibroblast interferon gene. A;Reference number: A93225; MUID:80254542; PMID:6157094

A; Accession: A93225

A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-187 -CDEN.
A; Kresidues: 1-187 -CDEN.
A; Cross-references: UNIPARC: UDI000004775D; GB: V00546; NID: 932735; PIDN: CAA23807.1; PID: 95; A; Cross-references: UNIPARC: UDI00004775D; GB: V00546; NID: 3285-2884, 1980
A; Houghton, M.; Baton, M.A.W.; Stewart, A.G.; Smith, J.C.; Doel, S.M.; Cartlin, G.H.; Lev Nucleic Acids Res. B, 2885-2884, 1980
A; Title: The complete amino acid sequence of human fibroblast interferon as deduced using A; Reference number: A93706; MUID: 81053720; PMID: 6159580

A; Accession: A93706

A; Molecule type: mRNA A; Residues: 1-187 <HOU>

A;Cross-rences: UNIPARC:UP1000004775D; GB:J00218; GB:K00616; GB:M11029; NID:g184626; A;Cross-rences: UNIPARC:UP1000004775D; GB:J00218; GB:K00616; GB:M11029; NID:g184626; B;Houghton, M.; Stewart, A.G.; Doel, S.M.; Emtage, J.S.; Eaton, M.A.W.; Smith, J.C.; Pat Nucleic Acids Res. 8, 1913-1931, 1980

Nucleic Acids Res. 8, 1913-1931, 1980

A;Fitle: The amino-terminal sequence of human fibroblast interferon as deduced from reve A;Reference number: A93700; MUD:81053854; PMID:6159597

A; Molecule type: mRNA

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Local Similarity 59.0 nes 98; Conservative
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                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 71-161, Yv. 163-187 <SHE>
A; Residues: 71-161, Yv. 163-187 <SHE>
A; Cross-references: UNIPARC: UPI0000173665
A; Note: the loss of Cys-162 (and of the ability to form the essential disulfide bond) in
R; Utsumi, J.; Mizuno, Y.; Hosoi, K.; Okano, K.; Sawada, R.; Kajitani, M.; Sakai, I.; Nar
Eur. J. Blochem. 181, 545-553, 1989
A; Title: Characterization of four different mammalian-cell-derived recombinant human int
A; Reference number: S04479; MUID:89276336; PMID:2731537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-187 <RES>
A;Cross-references: UNIPARC:UPI000004775D; GB:M28622; NID:g184624; PIDN:AAA36040.1; PID:
C;Genetics:
                                                                                                                                                                                 R;Shepard, H.M.; Leung, D.; Stebbing, N.; Goeddel, D.V.
Nature 294, 563-565, 1981
A;Title: A single amino acid change in IFN-beta-1 abolishes its antiviral activity.
A;Reference number: A93269; MUID:82080683; PMID:6171735
A;Accession: A93269
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A,Status: preliminary
A,Molecule type: protein
A,Residues: 22-187 <UTS>
A,Cross-references: UNIPARC:UPI000002BE76
B,May, L.T.; Selgal, P.B.
J. Interferon Res. 5, 521-526, 1985
A,Title: On the relationship between human interferon alpha-1 and beta-1 genes.
A,Reference number: 156315; MUID:86035565; PMID:2414376
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                                                                                                        A,Title: Assignment of the disulphide bonds of leukocyte interferon. A,Fateference number: A93244; MUID:81133083; PMID:6162107
A,Contents: annotation; disulfide bond
R;Shepard, H.M.; Leung, D.; Stebbing, N.; Goeddel, D.V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;22-187/Product: interferon beta-1 #status experimental <MAT>
;52-162/Disulfide bonds: #status predicted
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100.0%; Pred. No. 5.6e-64;
ive 0; Mismatches 0;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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A)Generación (GDB:120522, OMIM:147640
A;Map position: 9p21-9p21
C;Superfamily: interferon alpha
A;Residues: 1-68 <HO2>
A;Cross-references: UNIPARC:UPI0000173664
R;Wetzel, R.
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Matches 166; Conservative
                                            A; wetzel, R. Nature 289, 606-607, 1981 A; Title: Agginner
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interferon beta-I precursor - horse
NyAlternate names: EqIRN-beta-I; type I interferon
C;Species: Equus caballus (domestic horse)
C;Species: Equus caballus (domestic horse)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: G24912
R;Himmler, A.; Hauptmann, R.; Adolf, G.R.; Swetly, P.
DNA 5, 345-356, 1986
A;Title: Molecular cloning and expression in Escherichia coli of equine type I interferor
A;Reference number: A90956; MUID:87053170; PMID:302299
A;Accession: G24912
A;Molecule type: mRNA
A;Residues: 1.186 **HINA
A;Cross-references: UNIPROT: P05012; UNIPARC: UPI000002C9FB; GB:M14546; NID:g164228; PIDN::
C;Superfamily: interferon alpha
C;Superfamily: interferon alpha
C;Keywords: antiviral; glycoprotein
F;1-21/Domain: signal sequence #status predicted <*MAT>
F;22-186/Product: interferon beta-I #status predicted
F;101,136/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A,Residues: 1-186 <LEU>
A,COSS-references: UNIPROT:P01576; UNIPARC:UPI000012D64C
A;Cross-references: UNIPROT:P01576; UNIPARC:UPI000012D64C
C;Superfamily: interferon alpha
C;Keywords: glycoprotein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;2-15/Pomain: interferon beta-2 #status predicted <MAT>
F;2-16/Pomailfide bonds: #status predicted
F;2-161/Disulfide bonds: #status predicted
F;131,173/Binding site: carbohydrate (Asn) (covalent) #status predicted
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59.0%; Pred. No. 1.3e-32;
cive 27; Mismatches 40;
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A;Molecule type: DNA
A;Residues: 1-184 <YOK>
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C;Species: Bos primigenius taurus (cattle)
C;Date: 15-Nov-1984 #sequence_revision 15-Nov-1984 #text_change 09-Jul-2004
Bio/Technology 2, 458-464, 1984
A;Title: The structure and bacterial expression of three distinct bovine interferon-beta
A;Reference number: A90097
A;Residues: 1-186 < LEUA
A,Title: The structure and bacterial expression of three distinct bovine interferon-beta
A,Reference number: A90097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSLH 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 MLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSLH 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYSLLIRFQQRQSLIKECQKLLGQLPSTSQHCLEARMDFQMPEEMKQEQOFQKEDAILVMYE 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 SYSLLRFQQRRSAEVCQKLLGQLHSTPQHCLEAKMDFQVPEEMNQAQQFRKEDAILVIYE 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 SYNLIGFLORSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIYE
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P01578; UNIPARC:UP1000012D64B
C;Superfamily: interferon alpha
C;Keywords: glycoprotein
F;1-21.Domain: signal sequence #status predicted <SIG>
F;22-186/Product: interferon beta-1 #status predicted <WAT>
F;22-161/bisulfide bonds: #status predicted
F;52-161/bisulfide sonds: #status predicted
                                                                                                                                                                                                                                                                                    F; 57-161/Disulfide bonds: #starus preutureu F; 131,173/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ij
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                                                                                                                                                                                                                                                                                                                                                   52.5%; Score 458.5; DB 1; Length 186; 53.3%; Pred. No. 3e-30; Live 35; Mismatches 41; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 LKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN 166
                                                                                                                                                                                                                                                         <MAT>
                                               A;Reference number: A90097
A;Accession: A01841
A;Molecule type: DNA
A;Residues: 1-186 (-1850)
A;Cross-references: UNIPROT: P01577; UNIPARC: UPI000012D64E
C;Superfamily: interferon alpha
C;Reywords: glycoprotein
F;22-186/Product: interferon beta-3 #status predicted <81G>F;22-161/Disulfide bonds: #status predicted <WAIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y Match
Local Similarity 51.5%;
nes 85; Conservative 30
                                                                                                                                                                                                                                                                                                                                                                                                               88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 88; Conserv
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A Sand Back Sand

interferon beta precursor - mouse C;Species: Mus musculus (house mouse) C;Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004

IVMSB

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C;Accession: S02020; S04201; A01839
R;Vodjdani, G; Coulombel, C; Doly, J.
J. 1988
C;Accession: G; Coulombel, C; Doly, J.
J. John Biol. 204, 221-231, 1988
A;Title: Structure and characterization of a murine chromosomal fragment containing the j A;Title: Structure and characterization of a murine chromosomal fragment containing the j A;Reference number: S02020; MUID:89125582; PMID:3221389
A;Reference number: S02020; MUID:89125582; PMID:3221389
A;Reference under: S02020; MUID:89125582; PMID:3221389
A;Reference number: UNIPROT: P01575; UNIPARC: UP10000022EE3; EMBL:X14029; NID:951550; PIDN: R;Ruga, T.; Fujita, T.; Taniguchi, T.
Nucleic Acids Res. 17, 3291, 1989
A;Reference number: S04201
A;Reference number: S04201
A;Reference number: S04201
A;Status: translation not shown
A;Reference number: UNIPARC: UP10000022EE3; EMBL:X14455; NID:951538; PIDN: CAA32C25.1; PID: R;Higashi, Y.; S0Kawa, Y.; Watenabe, Y.; Kawade, Y.; Ohno, S.; Takaoka, C.; Taniguchi, T.
R;Higashi, Y.; S0Kawa, Y.; Watenabe, Y.; Rawade, Y.; Ohno, S.; Takaoka, C.; Taniguchi, T.
J; Biol. Chem. 258, 9522-9529, 1983
A;Title: Structure and expression of a cloned cDNA for mouse interferon-beta.
A;Reference number: A;Reference number: A01839; MUID:8326575; PMID:6688252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: A01839
A;Molecule type: mRNA
A;Residues: 1-182 <HIG>
A;Cross-references: UNIPARC:UPI0000222EB3; GB:K00020; NID:g194113; PIDN:AAA37891.1; PID:ç GGenetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: JC5424
R;Yokoyama, S.; Ohishi, N.; Shamoto, M.; Watanabe, Y.; Yagi, K.
Biochem. Biophys. Res. Commun. 232, 698-701, 1997
A;Title: Isolation and expression of rat interferon beta gene and growth-inhibitory effect A;Reference number: JC5424; MUID:97271387; PMID:9126338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: UNIPROT: P70499; UNIPARC: UPI000012D652; DDBJ: D87919; NID: 91616938; PII C; Comment: This protein exhibits characteristic antiviral and antitumor activities. C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 EMLQNVFLVFRNNFSSTGWNETIVVRLLDELHQQTVFLKTVLEEK-QEERLTWEMSSTAL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSYNLLGFLORSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Map position: 4
C;Superfamily: interferon alpha
C;Superfamily: interferon alpha
C;Keywords: glycoprotein:
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-182/Product: interferon beta #status predicted <MAT>
F;50,90,97/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 184;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
39.2%; Score 342.5; DB 1;
Best Local Similarity 46.4%; Pred. No. 7.5e-21;
Matches 77; Conservative 27; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.4%; Score 335.5;
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interferon alpha-I-1 precursor - horse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 MRSFSSSANLOGRL 185
                                                                                                                                   Local Similarity
nes 55; Conserv
                                                                                                             Query Match
                                                                                                                                      Best Loc
Matches
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NyAlternate names: EqFNN-alpha-II-2; EqIFN-omega-2; type I interferon
NyAlternate names: EqFNN-alpha-II-2; EqIFN-omega-2; type I interferon
C;Species: Equue caballus (domestic horse)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: F24912
R;Himmler, A.; Hauptmann, R.; Adolf, G.R.; Swetly, P.
DNA 5, 345-356, 1986
A;Title: Molecular cloning and expression in Escherichia coli of equine type I interferon
A;Reference number: A90956; MUID:87053170; PMID:3022999
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N;Alternate names: EqFN-alpha-II-1; EqIFN-omega-1; type I interferon
N;Alternate names: EqFN-alpha-II-1; EqIFN-omega-1; type I interferon
C;Species: Equues caballus (domestic horse)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: E24912
R;Himmler, A: Hauptmann, R.; Adolf, G.R.; Swetly, P.
DNA 5, 345-356, 1986
A;Title: Molecular cloning and expression in Escherichia coli of equine type I interferon
A;Reference number: A90956; MUID:87053170; PMID:3022999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-195 <HIM>
A;Residues: 1-195 <HIM>
A;Cross-references: UNIPROT:P05002; UNIPARC:UPI00002CA65; GB:M14545; NID:g164217; PIDN:
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A Molecule type: DNA
A Molecule type: DNA
A Residues: 1-195 «HIM»
A Cross-references: UNIPROT:P05001; UNIPARC:UPI000002C9FC; GB:M14544; NID:g164230; PIDN:
C Superfamily: interference and your and you will be appropriate and you'ver all glycoprotein
F;1-23/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                         61 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120
                                                                                                                                                                                                                   80 VMLQNVPLVFRSNFSSTGWNETIVESLLDELHQQTELLEIILKEK-QEERLTWVTSTTTL 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 MLQQIFSLFHTERSSAAWNTTLLDELCTGLLRQLEDLDTCLEQEMGEESALGTVRPTLA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 MLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSLH 121
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                                                                                                                   22 IDYKQLQFRQSTSIRTCQKLLRQLNGRLN--LSYRTDFKIPMEVMHPSQMEKSYTAFAIQ
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                                  Gaps
                                  3;
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F;1-23/Domain: signal sequence #status predicted <SIG>
F;1-24/Domain: signal sequence #status predicted <MAT>
F;24-125,52-162/Disulfide bonds: #status predicted
F;24-122,52-162/Disulfide bonds: #status predicted
F;101/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                            121 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.1%; Score 289; DB 1; Length 195; 37.2%; Pred. No. 1.8e-16; Indels :ive 33; Mismatches 56; Indels
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                                                                                                                                                                                                                                                                                                                       63;
        2.8e-20;
45.8%; Pred. ....
                                76; Conservative
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          Similarity
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        Best Local
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CiAccession: A24312
R;Himmler, A.; Hauptmann, R.; Adolf, G.R.; Swetly, P.

BNA 5, 345-356, 1986
A;Title: Molecular cloning and expression in Escherichia coli of equine type I interferor
A;Reference number: A90956; MUID:87053170; PMID:3022999
A;Accession: A24912
A;Accession: A24912
A;Reference number: Himbar A2912
A;Recience number: Himbar A3912
A;Rocossion: A24912
C;Superfamily: interferon alpha
C;Superfamily: interferon alpha
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                                                                                                                                                                                                                                                                                                   52 CLKHRIDFREPQEQLDGRQFPEAQAISVLQEMLQQIVSLFHIERSSAAWNTILLDRILAG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85
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NyAlternate names: EGIFN-alpha-I-3; type I interferon
C;Species: Equus caballus (domestic horse)
C;Species: Equus caballus (domestic horse)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: C24912
R;Himmler, A; Haupptnann, R.; Adolf, G.R.; Swetly, P.
Byitte: Molecular cloning and expression in Escherichia coli of equine type
A;Reference number: A90956; MUID:87053170; PMID:3022999
A;Accession: C24912
A;Molecule type: DNA
A;Residues: 1-184 <HIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N,Alternate names: EqfRN-alpha-I-1; type I interferon
C;Species: Equus caballus (domestic horse)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                   65 NIFAIFRODSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSLHLKR
                                                                                                                                                                                                                                                                  31 CLKDRMNFDIPEEIKQLQQFQKEDAALTIYEMLQNIFAIFRQDSSSTGWNETIVENLLAN
                                                                                                                                                                                                                                                                                                                                                                                              91 VYHQINHLKTVLEBKLEKEDFTRGKLMSSLHLKRYYGRILHYLKAKEYSHCAWTIVRVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 LLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIYEMLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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F;24-195/Product: interferon alpha-II-1 #status predicted <MAT>
F;24-122,52-162/Disulfide bonds: #status predicted
F;101/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-184/Product: interferon alpha-I-l #status predicted <MAT>
F;24-122,52-162/Disulfide bonds: #status predicted
                                                                                                                                                                                                     53; Indels
                                                                                                                               30.7%; Score 268; DB 1;
larity 41.0%; Pred. No. 9.1e-15;
Conservative 26; Mismatches 53.
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A;Cross.references: UNIPROT: PD65015; UNIPARC: UPI0000047763; GB: X02957; NID: g32653; PIDN: C3 Pt. Cross.references: UNIPROT: PD65015; UNIPARC: UPI0000047763; GB: X02957; NID: g32653; PIDN: C3 Pt. C. Natl. Acad. Sci. U.S.A. 81, 6451-6455, 1984
A;Title: Human genomic library screened with 17-base oligonucleotide probes yields a nove A;Reference number: A22068; MUID: 85038533; PMID: 6387705
A;Accession: A22068
A;Molecule type: DNA
A;Residues: 1.189
A;Accession: V.M.; Jansone, I.; Tsimanis, A.; Vishnevsky, Y.; Apsalons, U.
J. Interferences: UNIPARC: UPI0000047763; GB: K02055; NID: g184620; PIDN: AAA52727.1; PID: gR;Gren, E.; Berzin, V.M.; Jansone, I.; Tsimanis, A.; Vishnevsky, Y.; Apsalons, U.
J. Interference number: 156313; MUID: 85056523; PMID: 6548765
A;Accession: I73334
A;Accession: I73334
A;Accession: I73334
A;Accession: I73334
A;Accession: I73334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-references: UNIPARC:UPI0000047763; GB:M28585; NID:g184643; PIDN:AAA36042.1; PID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 LLWQLNGRLEY--CLKDRMNFDIPEEIKQLQQFQKEDAALTIYEMLQNIFAIFRQDSSST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Green GDB: IFNA16
A;Cross-references: GDB:136357; OMIM:147580
A;Amap position: 9p22-9p22
A;Introns: #status absent
C;Superfamily: interferon alpha
C;Keywords: antiviral; cytckine; leukocyte
F;1-23,Domain: signal sequence #status predicted <SIG>F;24-189/Product: interferon alpha-1-16 #status predicted <MAT>F;24-122,52-162/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 29.8%; Score 260.5; DB 1; 1 Similarity 37.2%; Pred. No. 3.6e-14; 55; Conservative 30; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Status: preliminary; translated from GB/EMBL/DDBJ; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Residues: 1-189 <RES>
A;Cross-references: UNIE
C;Genetics:
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   A; Accession: G23753
A; Molecule type: DNA
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Best Local Si
Matches 55;
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N;Alternate names: EqIFN-alpha-I-4; type I interferon
C;Species: Equus caballus (domestic horse)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: D24912
R;Himmler, A.; Hauptmann, R.; Adolf, G.R.; Swetly, P.
DNA 5, 345-356, 1986
A;Title: Molecular cloning and expression in Escherichia coli of equine type I interferch number: A90956; MuID:87053170; PMID:3022999
A;Accession: D24912
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A;Cross-references: UNIPROT:P05005; UNIPARC:UPI000002CA64; GB:M14542; NID:g164222; PIDN: C;Superfamily: interferon alpha (C;Keywords: antiviral F;1-23/Domain: signal sequence #status predicted <SIG>F;1-23/Domain: signal sequence #status predicted <MAT>F;24-184/Product: interferon alpha-I-3 #status predicted <MAT>F;24-122,52-162/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Molecule type: DNA
A,Residues: 1-184 <HIM>
A,Cross-references: UNIPROT:P05006; UNIPARC:UPI00002CA66; GB:M14543; NID:g164224; PIDN:
C,Superfamily: interferon alpha
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NyAlternate names: HuIRN-alpha-I-16; interferon alpha-I-WA; type I interferon
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: G23753; A22068; Ī73334
R;Henco, K.; Brostus, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes, J.R.; Hochstadt, J.; I
J. Mol. Biol. 185, 227-260, 1985
A;Title: Structural relationship of human interferon alpha genes and pseudogenes.
A;Reference number: A92916; MUID:86037205; PMID:4057246
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                                                                                                                                                                                                                                                                                                                                                                                       40 LLGOMRRISPFS------CLKDRNDFGFPQEVFDGNOFRKPQAISAVHETIQ
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                                                                                                                                                                                                            Query Match
30.2%; Score 264; DB 1; Length 184;
Best Local Similarity 36.7%; Pred. No. 1.8e-14;
Matches 55; Conservative 29; Mismatches 52; Indels
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Best Local Similarity 36.7%
Matches 55; Conservative
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Indels

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Righten, E.Y.; Berzin, V.M.; Tgimanis, A.Y.; Apsalon, U.R.; Vishnevskii, Y.I.; Yansone, I. A.; Lozha, V.P.; Kavsan, V.M.; Efimov, V.A.; Sverdlov, B.D.
Dokl. Blochem. 269, 91-95, 1983
A;Title: A new type of leukocytic interferon.
A;Reference number: 137583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q14618; UNIPARC:UP10000072A19; EMBL:X00140; NID:g32726; PIDN C;Superfamily: interferon alpha
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                                                                     78 GWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSLHLKRYYGRILHYLKAKE 137
                                                                                                        20 LLWQLNGRLEY -- CLKDRMNFDIPEEIKQLQQFQKEDAALTIYEMLQNIFAIFRQDSSST 77
C;Species: Homo sapiens (man)
C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 09-Jul-2004
C;Accession: 137584
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159 YSPCAWEVVRAEIMRSFSFSTNLQKGLR 186
                                                                                                                                                                                                138 YSHCAWTIVRVEILRNFYFINRLTGYLR 165
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Interferon alpha-I-2 precursor - horse

NyAlternate names: EqIFN-alpha-I-2; type I interferon

C, Species: Equue caballus (domestic horse)

C, Species: Equue caballus (domestic horse)

C, Accession: B24912

R; Himmber, A.; Hauptmann, R.; Adolf, G.R.; Swetly, P.

DNA 5, 345-356, 1986

A; Title: Molecular cloning and expression in Escherichia coli of equine type I interferce

A, Reference number: A90956; MUID:87053170; PMID:3022999

A, Residues: 1-144 < LAID.

A, Residues: 1-144 < LAID.

A, Cross-reference: UNIPROT:P05004; UNIPARC:UPI000002C9FA; GB:M14541; NID:g164218; PIDN:

C, Superfamily: interferon alpha

C, Keywords: antivixal

F; 1-22/Domain: signal sequence #status predicted <SIG>
F; 24-184/Product: interferon alpha-I-2 #status predicted

F; 24-122, 52-162/Disulfide bonds: #status predicted
                                                                                      86 QIFHLFSIDGSSAAWDESLLDXLYTGLYQQLTELEACLSQEVGYEETPLMNEDSLLAVRR 145
                                                     GWNETIVENLLANVYHQINHLKTVLBEKLEKEDFTRGKLMSSLHLKRYYGRILHYLKAKE 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 NIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSLHLKR 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64
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40 LLAQM-GRISHFSCLKDRYDFGFPQEVFDGNQFQKAQAISAFHEMIQQTFNLFSTKDSSA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 LLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIYEMLQ
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                                                                                                                                                          138 YSHCAWTIVRVEILRNFYFINRLTGYLR 165
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